

**AMENDMENT**

Claims 46-91 are pending in this application. Please amend claims 55, 63, 70, 74, 79, and 80 as follows, without prejudice to their further prosecution, as shown below in the complete listing of the claims.

1-45. (Cancelled)

46. (Previously presented) An automated method for identifying a component in a DNA sample, comprising:

using a mass spectrometer to generate a computer readable data set comprising data representing components in the biological sample for analysis by a computer, and using the computer to:

denoise the data set to generate denoised data;  
correct a baseline from the denoised data to generate an intermediate data set;  
define putative peaks in the intermediate data set, wherein the putative peaks represent components in the DNA sample;  
generate a residual baseline by removing the putative peaks from the intermediate data set;  
remove the residual baseline from the intermediate data set to generate a corrected data set;  
locate a putative peak in the corrected data set; and  
identify the component that corresponds to the located putative peak.

47. (Previously presented) The method of claim 46, wherein said mass spectrometer is a MALDI-TOF mass spectrometer.

48. (Previously presented) The method according to claim 46 wherein denoising the data set includes generating a noise profile for the data set.

49. (Previously presented) The method according to claim 46 wherein denoising the data set includes transforming the data set using wavelet technology into a series of stages.

50. (Previously presented) The method according to claim 49 further including generating a noise profile for stage 0.

51. (Previously presented) The method according to claim 50 further including generating a noise profile for other stages.

52. (Previously presented) The method according to claim 51 wherein the noise profile for each of the other stages is the noise profile for stage 0 scaled by a scaling factor

53. (Previously presented) The method according to claim 52 wherein the scaling factor is derived from the end portion of each of the other stages, respectively.

54. (Previously presented) The method according to claim 49 further including applying a threshold to selected stages, the threshold being derived from the noise profile.

55. (Currently amended) The method according to claim ~~of~~ 54 wherein the threshold is scaled by a threshold factor before being applied to the selected stages.

56. (Previously presented) The method according to claim 55 wherein the threshold factor is selected so that higher stages of data are filtered less than lower stages.

57. (Previously presented) The method according to claim 49 further including generating a sparse data set indicative of the denoised data.

58. (Previously presented) The method according to claim 49 further including shifting the denoised data to account for variations due to a starting value for the wavelet transformation.

59. (Previously presented) The method according to claim 46 wherein correcting the baseline further includes generating a moving average of the denoised data set.

60. (Previously presented) The method according to claim 59 wherein the moving average is used to find peak sections in the denoised data set.

61. (Previously presented) The method according to claim 60 wherein the peak sections are removed from the denoised data set.

62. (Previously presented) The method according to claim 61 further including generating a baseline correction.

63. (Currently amended) ~~The method according to claim 46 further including~~  
An automated method for identifying a component in a DNA sample, comprising:  
using a mass spectrometer to generate a computer readable data set comprising data  
representing components in the biological sample for analysis by a computer, and using the computer  
to:

denoise the data set to generate denoised data;

correct a baseline from the denoised data to generate an intermediate data set;

define putative peaks in the intermediate data set, wherein the putative peaks  
represent components in the DNA sample;

compressing the intermediate data set, the intermediate data set having a plurality  
of data values associated with respective points in an array of data;

generate a residual baseline by removing the putative peaks from the intermediate  
data set;

remove the residual baseline from the intermediate data set to generate a corrected  
data set;

locate a putative peak in the corrected data set; and

identify the component that corresponds to the located putative peak.

64. (Previously presented) The method according to claim 63 wherein a compressed data value is a real number that includes a whole portion representing the difference between two

points in an array of data.

65. (Previously presented) The method according to claim 63 wherein a compressed data value is a real number that includes a decimal portion representing the difference between a maximum value of all the data values and a value at a particular point in an array.

66. (Previously presented) The method according to claim 46 further including performing a mass shift based on the position of the putative peaks.

67. (Previously presented) The method according to claim 46 wherein generating the residual baseline includes deleting an area around each putative peak in the intermediate data set.

68. (Previously presented) The method according to claim 67 wherein the area deleted is derived from a determined width of a putative peak.

69 (Previously presented) The method according to claim 67 wherein the residual baseline is derived from data remaining in the intermediate data set after the areas around the putative peaks have been removed.

70. (Currently amended) ~~The method according to claim 69,~~  
An automated method for identifying a component in a DNA sample, comprising:  
using a mass spectrometer to generate a computer readable data set comprising data  
representing components in the biological sample for analysis by a computer, and using the computer  
to:

denoise the data set to generate denoised data;

correct a baseline from the denoised data to generate an intermediate data set;

define putative peaks in the intermediate data set, wherein the putative peaks  
represent components in the DNA sample;

generate a residual baseline by removing the putative peaks from the intermediate  
data set;

remove the residual baseline from the intermediate data set to generate a corrected data set;  
locate a putative peak in the corrected data set; and  
identify the component that corresponds to the located putative peak;  
wherein generating the residual baseline includes deleting an area around each putative peak in the intermediate data set; the residual baseline is derived from data remaining in the intermediate data set after the areas around the putative peaks have been removed; and

wherein an area equal to twice the width of the Gaussian is removed from the left of the center line of the putative peaks.

71. (Previously presented) The method according to claim 69, wherein an area equivalent to 50 daltons is removed from the right of the center line of the putative peaks.

72. (Previously presented) The method according to claim 67 wherein generating the residual baseline includes fitting a quartic polynomial to the data set remaining in the intermediate data after the peaks have been removed.

73. (Previously presented) The method according to claim 46 wherein the putative peak is located by fitting a Gaussian curve to a peak area in the corrected data set.

74. (Currently amended) ~~The method according to claim 46~~

An automated method for identifying a component in a DNA sample, comprising:  
using a mass spectrometer to generate a computer readable data set comprising data  
representing components in the biological sample for analysis by a computer, and using the  
computer to:

denoise the data set to generate denoised data;  
correct a baseline from the denoised data to generate an intermediate data set;  
define putative peaks in the intermediate data set, wherein the putative peaks  
represent components in the DNA sample;

generate a residual baseline by removing the putative peaks from the intermediate data set;  
remove the residual baseline from the intermediate data set to generate a corrected data set;  
locate a putative peak in the corrected data set; and  
identify the component that corresponds to the located putative peak;

wherein the identifying step includes using a generated noise profile to calculate the signal-to-noise ratio for the putative peak.

75. (Previously presented) The method according to claim 74 wherein a residual peak error is calculated by comparing the putative peak to a Gaussian curve.

76. (Previously presented) The method according to claim 75 wherein the residual peak error is used to adjust the signal-to-noise ratio to generate an adjusted signal-to-noise ratio.

77. (Previously presented) The method according to claim 46 wherein the identifying step includes deriving a peak probability for the putative peak.

78. (Previously presented) The method according to claim 77 wherein the peak probability is derived using the signal-to-noise ratio.

79. (Currently amended) ~~The method according to claim 78~~  
An automated method for identifying a component in a DNA sample, comprising:  
using a mass spectrometer to generate a computer readable data set comprising data  
representing components in the biological sample for analysis by a computer, and using the  
computer to:  
denoise the data set to generate denoised data;  
correct a baseline from the denoised data to generate an intermediate data set;

define putative peaks in the intermediate data set, wherein the putative peaks represent components in the DNA sample;  
generate a residual baseline by removing the putative peaks from the intermediate data set;  
remove the residual baseline from the intermediate data set to generate a corrected data set;  
locate a putative peak in the corrected data set; and  
identify the component that corresponds to the located putative peak;

wherein the identifying step includes deriving a peak probability for the putative peak, and wherein peak probability is derived by using an allelic ratio, the allelic ratio being a comparison of two peak heights indicated in the corrected data.

80. (Currently amended) ~~The method according to claim 46~~

An automated method for identifying a component in a DNA sample, comprising:  
using a mass spectrometer to generate a computer readable data set comprising data representing components in the biological sample for analysis by a computer, and using the computer to:

denoise the data set to generate denoised data;  
correct a baseline from the denoised data to generate an intermediate data set;  
define putative peaks in the intermediate data set, wherein the putative peaks represent components in the DNA sample;  
generate a residual baseline by removing the putative peaks from the intermediate data set;  
remove the residual baseline from the intermediate data set to generate a corrected data set;  
locate a putative peak in the corrected data set; and  
identify the component that corresponds to the located putative peak;

wherein the identifying step includes calculating a peak probability that a putative peak in the corrected data is a peak indicating composition of the DNA sample.

81. (Previously presented) The method according to claim 80 wherein peak probability is calculated for each of a plurality of putative peaks in the corrected data.

82. (Previously presented) The method according to claim 81 wherein a highest probability is compared to a second-highest probability to generate a calling ratio.

83. (Previously presented) The method according to claim 82 wherein the calling ratio is used to determine if the composition of the DNA\_sample will be called.

84. (Previously presented) A computerized system for identifying a component in a DNA sample, the system comprising:

an instrument for receiving the DNA\_sample and generating a data set capable of analysis by a computer comprising data representing components in the DNA sample;

a computer communicating with the instrument and configured to receive the generated data set, the computer programmed to perform the method of:

denoising the data set to generate denoised data;

correcting a baseline from the denoised data to generate an intermediate data set;

defining putative peaks in the intermediate data set, wherein the putative peaks represent components in the sample;

generating a residual baseline by removing the putative peaks from the intermediate data set;

removing the residual baseline from the intermediate data set to generate a corrected data set;

locating a putative peak in the corrected data set; and

identifying the component that corresponds to the located putative peak.

85. (Previously presented) The system according to claim 84 wherein the computer is integral to the instrument.



86. (Previously presented) A machine readable program operating on a computing device, the computing device being configured to receive a data set comprising computer readable data representing components of a DNA sample, wherein the program directs the computing device to implements the steps of:

- denoising the data set to generate denoised data;
- correcting a baseline from the denoised data to generate an intermediate data set;
- defining putative peaks in the intermediate data set, wherein the putative peaks represent components in the DNA sample;
- generating a residual baseline by removing the putative peaks from the intermediate data set;
- removing the residual baseline from the intermediate data set to generate a corrected data set;
- locating a putative peak in the corrected data set; and
- identifying the component that corresponds to the located putative peak.

87. (Previously presented) A system for identifying a component of a DNA sample, comprising:

- a mass spectrometer for receiving the DNA sample and generating a computer readable data set comprising data representing components in the DNA sample;

- a computing device configured to receive the computer readable data set, the computing device programmed to implement the method comprising:

- denoising the data set to generate denoised data;
- correcting a baseline from the denoised data to generate an intermediate data set;
- defining putative peaks in the intermediate data set, wherein the putative peaks represent components in the DNA sample;
- generating a residual baseline by removing the putative peaks from the intermediate data set;
- removing the residual baseline from the intermediate data set to generate a corrected data set;
- locating a putative peak in the corrected data set; and
- using the located putative peak to identify the component that corresponds thereto.

88. (Previously presented) The system according to claim 87, where the method further includes using a statistical methodology to determine if the located putative peak is an actual peak.

89. (Previously presented) The system according to claim 88, where the method further includes determining whether a probability of the actual peak existing is sufficiently high to identify the component of the DNA sample, and if the probability is not sufficiently high, then the method does not identify the component.

90. (Previously presented) The system according to claim 89, where the percentage of correctly called components is about 100 percent.

91. (Previously presented) A system for identifying a component in a DNA sample, comprising:

- an instrument receiving the DNA sample and generating a computer readable data set indicative of the component in the DNA sample;

- a computing device for receiving the computer readable data set and performing the steps of:
  - generating an intermediate data set by processing the data set to remove noise due to system and chemical reaction characteristics, the intermediate data set having putative peak areas;

- defining the position of expected peaks using known possible peak areas from the DNA sample;

- shifting the intermediate data set to more closely align the putative peaks to the expected peaks;

- generating a residual baseline by removing the putative peaks from the shifted data set;

- removing the residual baseline from the shifted data set to generate a corrected data set;

- calculating the probability that each of the putative peaks in the corrected data set are actual peaks;

- comparing the highest probability to the second-highest probability to generate a calling ratio; and

using the calling ratio to determine if the identity of the component of the DNA sample is called.